A METHOD FOR GENERATING HYPERMUTABLE PLANTS

This application claims the benefit of provisional application Serial No. 60/183,333, filed February 18, 2000.

TECHNICAL FIELD OF THE INVENTION

The invention is related to the area of mismatch repair genes. In particular it is related to the field of mutagenesis.

BACKGROUND OF THE INVENTION

Within the past four years, the genetic cause of the Hereditary Nonpolyposis Colorectal Cancer Syndrome (HNPCC), also known as Lynch syndrome II, has been ascertained for the majority of kindreds affected with the disease (1). The molecular basis of HNPCC involves genetic instability resulting from defective mismatch repair (MMR). To date, six genes have been identified in humans that encode proteins which appear to participate in the MMR process, including the *mutS* homologs *GTBP, hMSH2,* and *hMSH3* and the *mutL* homologs *hMLH1*, *hPMS1*, and *hPMS2* (2-7). Germline mutations in four of these genes (*hMSH2*, *hMLH1*, *hPMS1*, and *hPMS2*) have been identified in HNPCC kindreds (2-7). Though the mutator defect that arises from the MMR deficiency can affect any DNA sequence, microsatellite sequences are particularly sensitive to MMR abnormalities (8,9). In addition to its occurrence in virtually all tumors arising in HNPCC patients, Microsatellite Instability (MI) is found in a small fraction of sporadic tumors with distinctive molecular and phenotypic properties (10).

HNPCC is inherited in an autosomal dominant fashion, so that the normal cells of affected family members contain one mutant allele of the relevant MMR gene (inherited from an affected parent) and one wild-type allele (inherited from the unaffected parent). During the early stages of tumor development, however, the wild-type allele is inactivated through a somatic mutation, leaving the cell with no functional MMR gene and resulting in a profound defect in MMR activity. Because a somatic

mutation in addition to a germ-line mutation is required to generate defective MMR in the tumor cells, this mechanism is generally referred to as one involving two hits, analogous to the biallelic inactivation of tumor suppressor genes that initiate other hereditary cancers. In line with this two-hit mechanism, the non-neoplastic cells of HNPCC patients generally retain near normal levels of MMR activity due to the presence of the wild-type allele (11-12).

While MMR is a conserved process found in bacteria, yeast, and mammalian cells (14-16), its activity has not been confirmed in plants. While sequences homologous to MMR genes have been identified in Arabidopsis thaliana, it is not known if they are functional in plants in the process of MMR (17-18). There is a need in the art for identification of the processes involved in genome stability in plants. There is a continuing need for methods and techniques for generating genetic diversity in agriculturally important crops.

SUMMARY OF THE INVENTION

It is an object of the invention to provide a method for making a hypermutable cell.

It is another object of the invention to provide a homogeneous composition of cultured, hypermutable, plant cells.

It is still another object of the invention to provide a hypermutable transgenic plant.

It is yet another object of the invention to provide a method for generating a mutation in a gene of interest in a plant cell.

It is still another object of the invention to provide a method for generating a mutation in a gene of interest in a plant.

It is an object of the invention to provide a method for generating a hypermutable plant.

It is another object of the invention to provide a vector for introducing a dominant negative MMR allele into a plant.

It is even another object of the invention to provide an

isolated and purified polynucleotide encoding a plant MutL homolog.

It is another object of the invention to provide an isolated and purified protein which is a plant MutL homolog.

It is an object of the invention to provide a method for determining the presence of a mismatch repair (MMR) defect in a plant or a plant cell.

These and other objects of the invention are provided by one or more of the following embodiments. In one embodiment of the invention a method for making a hypermutable cell is provided. A polynucleotide comprising a dominant negative allele of a mismatch repair gene is introduced into a plant cell, whereby the cell becomes hypermutable.

In another aspect of the invention a homogeneous composition of cultured, hypermutable, plant cells is provided. The plant cells comprise a dominant negative allele of a mismatch repair gene.

Another aspect of the invention is a hypermutable transgenic plant. At least 50% of the cells of the plant comprise a dominant negative allele of a mismatch repair gene.

According to another aspect of the invention a method is provided for generating a mutation in a gene of interest in a plant cell. A hypermutable plant cell comprising the gene of interest and a dominant negative allele of a mismatch repair gene is grown. The cell is tested to determine whether the gene of interest harbors a newly acquired mutation.

Another embodiment of the invention is a method for generating a mutation in a gene of interest in a plant. A plant comprising the gene of interest and a polynucleotide encoding a dominant negative allele of a mismatch repair gene is grown. The

plant is tested to determine whether the gene of interest harbors a newly acquired mutation.

According to another aspect of the invention a method is provided for generating a hypermutable plant. Endogenous mismatch repair (MMR) activity of a plant is inhibited. The plant becomes hypermutable as a result of the inhibition.

Another aspect of the invention is a vector for introducing a dominant negative MMR allele into a plant. The vector comprises a dominant negative MMR allele under the transcriptional control of a promoter which is functional in a plant.

Still another aspect of the invention provides an isolated and purified polynucleotide encoding Arabidopsis thaliana PMS2 as shown in SEQ ID NO: 14.

Another aspect of the invention provides an isolated and purified polynucleotide encoding Arabidopsis PMS134 as shown in SEQ ID NO: 16.

According to another embodiment of the invention an isolated and purified protein which is Arabidopsis PMS2 is provided. It has the amino acid sequence as shown in SEQ ID NO: 14.

Another embodiment of the invention is an isolated and purified protein which is Arabidopsis PMS134. It has the amino acid sequence as shown in SEQ ID NO: 16.

Still another aspect of the invention provides a method for determining the presence of a mismatch repair (MMR) defect in a plant or a plant cell. At least two microsatellite markers in test cells or a test plant are compared to the at least two microsatellite markers in cells of a normal plant. The test plant or plant cells are identified as having a mismatch repair defect if at least two microsatellite markers are found to be rearranged relative to the cells of the normal plant.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1. Alignment of the Arabidopsis thaliana and human PMS2 cDNAs.

Fig. 2. Alignment of the Arabidopsis thaliana and human PMS2 proteins.

Fig. 3. Alignment of the Arabidopsis thaliana MLH1 homolog and the human PMS2 proteins.

Fig. 4. Alignment of the Arabidopsis thaliana PMS1 homolog and the human PMS2 proteins.

Fig. 5. Phylogenetic tree of Arabidopsis thaliana MutL homologs and the human PMS2 protein.

Fig. 6. Alignment of the Arabidopsis thaliana PMS134 and the human PMS134 cDNA.

Fig. 7. Alignment of the Arabidopsis thaliana PMS134 and the human PMS134 polypeptides.

Fig. 8. Western blot analysis of bacteria expressing the hPMS134 (Fig. 8A) or the Arabidopsis thaliana PMS134 (Fig. 8B) polypeptides.

Fig. 9. Expression of plant dominant negative MMR genes produces hypermutability in bacteria, demonstrating the functionality of plant MMR proteins.

Fig. 10. Schematic diagram of a plant dominant-negative MMR expression vector.

Fig. 11. Transgenic plants containing the PMS134-KAN vector express the dominant negative hPMS134 gene.

Fig. 12. Microsatellite instability in plants expressing dominant negative MMR hPMS134 gene.

Fig. 13. MMR defective plants produce new phenotypes. Plants with decreased MMR produce offspring with two shoot apical meristems (SAM) in contrast to control plants exhibiting a single SAM.

DETAILED DESCRIPTION OF THE INVENTION

It is a discovery of the present inventors that plant cells have functional mismatch repair (MMR) systems which function similarly to mammalian MMR. Moreover, dominant negative alleles can be made and used to generate variability in plants and plant cells, as in mammalian cells. Other means of interfering with normal MMR activity can also be used as described in detail below. Dominant negative alleles of mismatch repair genes, when introduced into cells or plants, increase the rate of spontaneous or induced mutations by reducing the effectiveness of DNA repair and thereby render the cells or whole organism hypermutable. Hypermutable plant cells or plants can be utilized to develop new mutations in a gene of interest.

The process of mismatch repair, also called mismatch proofreading, is carried out by protein complexes in cells ranging from bacteria to mammalian cells (9, 14-16). A mismatch repair (MMR) gene is a gene that encodes one of the proteins of a mismatch repair complex. Although not wanting to be bound by any particular theory or mechanism of action, a mismatch repair complex is believed to detect distortions of a DNA helix resulting from non-complementary pairing of nucleotide bases. The non-complementary base on the newer DNA strand is excised, and the excised base is replaced with the appropriate base, which is complementary to the older DNA strand. In this way, cells eliminate many mutations which occur as a result of mistakes in DNA replication.

For purposes of example, this application discloses use of dominant negative alleles of MMR genes as a method for blocking or inhibiting MMR activity in plants. (Blocking or inhibiting are used synonymously herein, and denote any significant level of inhibition. They do not connote complete inhibition, although the terms include that possibility within their ambit.) However, any molecular method known by those skilled in the art to block MMR gene expression and/or function can be used, including but not limited to gene knockout (19), antisense technology (20), double stranded RNA interference (21), and polypeptide inhibitors (22).

Dominant negative alleles cause a mismatch repair defective phenotype even in the presence of a wild-type allele in the same cell. An example of a dominant negative allele of a mismatch repair gene is the human gene *hPMS2-134*, which carries a truncation mutation at codon 134 (13, U.S. Patent No. 6,146,894). The mutation causes the product of this gene to prematurely terminate at the position of the 134th amino acid, resulting in a shortened polypeptide containing the N-terminal 133 amino acids. Such a mutation causes an increase in the rate of mutations which accumulate in cells after DNA replication. Expression of a dominant negative allele of a mismatch repair gene results in impairment of mismatch repair activity, even in the presence of the wild-type allele. Any allele which produces such effect can be used in this invention.

Dominant negative alleles of a mismatch repair gene can be obtained from the cells of humans, animals, yeast, bacteria, plants or other organisms as described by Nicolaides et. al. (23) and Hori et. al. (24). Alternatively such alleles can be made from wild-type alleles, typically by inserting a premature stop codon or other mutation which leads to a protein product which is able to complex with other members of the MMR complex but which is not functional. Such alleles can be identified by screening cells for defective mismatch repair activity. The cells may be mutagenized or not. Cells from plants exposed to chemical mutagens or radiation, *e.g.*, can be screened for defective mismatch repair. Genomic

DNA, a plasmid containing cDNA, or mRNA from any cell encoding a mismatch repair protein can be analyzed for variations from the wild type sequence. Dominant negative alleles of a mismatch repair gene can also be created artificially, for example, by producing variants of the *hPMS2-134* allele or other mismatch repair genes (13, U.S. Patent No. 6,146,894). Other truncated alleles of *PMS2* or other MMR genes can be made. Such alleles are expected to behave similarly to *hPMS2-134*. An of various forms of site-directed mutagenesis can be used. The suitability of such alleles, whether natural or artificial, for use in generating hypermutable cells or plants can be evaluated by testing the mismatch repair activity caused by the allele in the presence of one or more wild-type alleles, to determine if the allele is dominant negative.

A cell or a plant into which a dominant negative allele of a mismatch repair gene has been introduced will become hypermutable. This means that the mutation rate (spontaneous or induced) of such cells or plants is elevated compared to cells or plants without such alleles. The degree of elevation of the mutation rate can be at least 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold, 200-fold, 500-fold, or 1000-fold that of the normal cell or plant.

According to one aspect of the invention, a polynucleotide encoding a dominant negative form of a mismatch repair protein is introduced into a cell or a transgenic plant. The gene can be any dominant negative allele encoding a protein which is part of a mismatch repair complex, for example, *mutS or mutL* homologs of the bacterial, yeast, fungal, insect, plant, or mammalian genes. The dominant negative allele can be naturally occurring or made in the laboratory. The polynucleotide can be in the form of genomic DNA, cDNA, RNA, or a chemically synthesized polynucleotide. The polynucleotide can be introduced into the cell by transfection.

Transfection is any process whereby a polynucleotide is introduced into a cell. The process of transfection can be carried out in a living plant,

e.g., using a binary vector for gene transmission, or it can be carried out *in vitro*, *e.g.*, using a suspension of one or more isolated cells in culture. The cell can be any type of plant cell.

In general, transfection can be carried out using a suspension of cells, or a single cell, but other methods can also be used as long as a sufficient fraction of the treated cells incorporates the polynucleotide to allow transfected cells to be readily isolated. The protein product of the polynucleotide may be transiently or stably expressed in the cell. Techniques for transfection are well known in the art of plant cell science. Available techniques for introducing polynucleotides include but are not limited to electroporation, transduction, Agrobacterium-mediated gene transfer, cell fusion, the use of calcium chloride, and packaging of the polynucleotide together with lipid for fusion with the cells of interest. Once a cell has been transfected with the mismatch repair gene, the cell can, *e.g.*, be grown and reproduced in culture. If the transfection is stable, such that the gene is expressed at a consistent level for many cell generations, then a cell line results. Alternatively, a dominant negative MMR protein can be directly introduced by microinjection into a cell in order to inhibit MMR activity of the cell.

Root explants are incubated in 0.5 ug/ml of 2-4-dochlorophenoxy-acetic acid (2-4D) plus N6-Benzyl-Adenine in growth medium. After 4 weeks, suspension cells are isolated and digested with hemicellulase for protoplast preparation and transfection. Such isolated cells are typically cultured in the absence of other types of cells. Cells selected for the introduction of a dominant negative allele of a mismatch repair gene may be derived from a multicellular plant in the form of a primary cell culture or an immortalized cell line, or may be derived from suspensions of single-celled plants.

A polynucleotide encoding a dominant negative form of a mismatch repair protein can be introduced into the genome of a plant to form a transgenic plant. The plant can be any species for which suitable

techniques are available to produce transgenic plants. For example, transgenic plants can be prepared from domestic agricultural crops, *e.g.* corn, wheat, soybean, rice, sorghum, barley, etc.; from plants used for the production of recombinant proteins, *e.g.*, tobacco leaf; or experimental plants for research or product testing, *e.g.*, *Arabidopsis*, pea, *etc.* The introduced polynucleotide may encode a protein native to the species or native to another species, whether plant, animal, bacterial, or fungal, for example.

Any method for making transgenic plants known in the art can be used. According to one process of producing a transgenic plant, the polynucleotide is transfected into the plant seedling The seed is germinated and develops into a mature plant in which the polynucleotide is incorporated and expressed. An alternative method for producing transgenic plants involves introducing the polynucleotide into the growing or mature plant by injection, electroporation, Agrobacterium-mediated transfer or transfection. With this method, if the polynucleotide is not incorporated into germline cells, the gene will not be passed on to the progeny. Therefore, a transgenic plant produced by this method will be useful to produce products from that individual plant.

To identify whether a gene was inserted into the germline, seedlings derived from such plants can be screened for the transgene. Genetic modification of a growing or mature plant is useful for evaluating the expression of hypermutable constructs and for evaluating effects on altering endogenous mismatch repair. Once transgenic plants are produced, they can be grown to produce and maintain a crop of transgenic plants.

Once a transfected cell line or a crop of transgenic plants has been produced, it can be used to generate new mutations in one or more gene(s) of interest. A gene of interest can be any gene naturally possessed by the cell line or transgenic plant or introduced into the cell line or transgenic plant. An advantage of using MMR-defective cells or plants to induce mutations is that the cell or plant need not be exposed to mutagenic

chemicals or radiation, which may have secondary harmful effects, both on the object of the exposure and on the workers.

Mutations can be detected by analyzing the genotype of the cells or plants, for example by examining the sequence of genomic DNA, cDNA, messenger RNA, or amino acids associated with the gene of interest. Mutations can also be detected by testing a phenotype caused by the gene. A mutant phenotype can be detected, *e.g.*, by identifying alterations in electrophoretic mobility, spectroscopic properties, or other physical or structural characteristics of a protein encoded by a mutant gene. One can also screen for altered function of the protein *in situ*, in isolated form, or in model systems. One can screen for alteration of any property of the cell or plant associated with the function of the gene of interest or its protein product. Finally, one can screen for macroscopic phenotypes such as but not limited to color, height, or the ability to grow in drought, high-salt, cold, hot, acidic, basic, pest-infested, or high ethylene environments.

The above disclosure generally describes the present invention. A more complete understanding can be obtained by reference to the following specific examples that will be provided herein for purposes of illustration only, and are not intended to limit the scope of the invention.

EXAMPLE 1: Isolation of Plant Mismatch Repair Genes.

The ability to increase the hypermutability of host genomes has many commercial and medical applications. The generation of hypermutable plants such as those used in agriculture for livestock feed and human consumption are just one example of many types of applications that can be generated by creating hypermutable organisms. For instance, the creation of crops that are less susceptible to pests or soil pH would greatly increase yield of certain agricultural crops. In addition to greater production of goods, improved crops could increase the ability to grow many generations of crops on the same fields (25-27). Moreover, the

ability to affect certain growth traits such as natural pest-resistance, drought-resistance, frost-resistance, increased production, or altered stalk size has many benefits for the production of agricultural products. Recently, it has been demonstrated that genes affecting the biologic activity of the plant growth hormone gibberellin results in crops with shorter stalk length that produce similar amounts of grain yields, however, the fact that the stalks are shorter makes these plants less susceptible to high winds and crop damage (28). The use of hypermutable crops could allow for the selection of shorter plants across many species such as corn, rice, etc, without having to first identify a gene to alter its activity. Another application of hypermutable agricultural products is the generation of crops with enhanced levels of vitamins and nutrients. One can select for enhanced vitamin production in seedlings of MMR defective plants. Recently, it has been demonstrated that altering a gene(s) within a vitamin biosynthetic pathway can result in the production of elevated levels of vitamin E (27,29).

Applications of hypermutable plants include use as crops for agricultural production, increased medicinal entities within plant extracts, chemicals and resins for industrial use, and their use as detoxifying organisms for environmental applications as described (25,26,29).

MutS and mutL homologs can be isolated from plant species libraries using degenerate RT-PCR, and standard Southern hybridization techniques as previously described (3,23,30). These may serve as reagents for producing MMR defective plant hosts. This process employs methods known by those skilled in the art of gene cloning.

One such approach is the use of degenerate PCR to clone MutS homologs following the methods used by Leach et. al. to clone the human MSH2 (3). Additional degenerate oligonucleotides can be generated and used against conserved domains of bacterial, yeast, and human MutS homologs. Various plant species cDNAs (obtainable from various commercial sources) can be amplified for MutS gene homologs by

polymerase chain reaction (PCR). Products are cloned into T-tailed vectors (In Vitrogen) and analyzed by restriction endonuclease digestion. Clones with expected DNA fragment inserts are sequenced using M13 forward and reverse primers located on the vector backbone flanking the cloning site. Fragments containing MMR gene homologs are then used as probes to screen commercially available cDNA libraries from the appropriate species. cDNA contigs are generated to create a cDNA containing the sequence information for the full length MMR gene and its encoded polypeptide. One such example of cloning a plant MMR gene is provided below.

In order to clone mutL homologs, degenerate primers were synthesized to the conserved domains of the mutL gene family by aligning *E. coli*, yeast, mouse, and human *mutL* genes. These primers are directed to the polynucleotide sequences centered at nt 150 to 350 of the published human PMS2 cDNA (SEQ ID NO: 3). Degenerate PCR was carried out using RNA from Arabidopsis thaliana (AT) that was isolated using the RNeasy kit following the manufacturer's protocol (Qiagen). RNAs were reverse transcribed (RT) using SuperscriptII (Life Technologies) following the manufacturer's protocol. After RT, cDNAs were PCR amplified using degenerate primers in buffers described by Nicolaides et. al. 1995 (23,30), and reactions were carried out at 95°C for 30 sec for 1 cycle followed by 94°C for 30 sec, 45°C for 60 sec, and 72°C for 60 sec for 20 cycles. PCR reactions were then diluted 1:10 in water and reamplified using the same primers and buffers. The secondary PCR reactions were carried out at 95°C for 30 sec for 1 cycle followed by 94°C for 30 sec, 52°C for 90 sec, and 72°C for 90 sec for 35 cycles. Reactions were analyzed by agarose gel electrophoresis. Products of the expected molecular weight were excised and cloned into T-tailed vectors (InVitrogen). Recombinant clones were sequenced and blasted against the public databases. The homolog was found to have homology to the mutL family of genes. Blast search analysis of GenBank found this gene to be part of a "putative" mismatch repair gene identified from the Arabidopsis genome project that has never been

reported to be transcribed or capable of producing a message. In order to clone the full length, an Arabidopsis cDNA library was screened by PCR as well as cDNA from AT plants using 5' primers corresponding to the initiation codon (SEQ ID NO: 1: 5'-atg caa gga gat tct tc-3') and the termination codon (SEQ ID NO: 2: 5'-tca tgc caa tga gat ggt tgc-3') using buffers and conditions listed above. Amplifications were carried out at 95°C for 30 sec for 1 cycle followed by 94°C for 30 sec, 58°C for 2 min, and 72°C for 3 min for 35 cycles. Products were analyzed by gel electrophoresis. Products of the expected molecular weights were subcloned into T-tail vectors and sequenced using primers from the cloning vector or using internal primers. Figure 1 shows the alignment of one Arabidopsis homolog, referred to as *ATPMS2* (SEQ ID NO: 4), to the human *PMS2* cDNA (SEQ ID NO:3) (Fig. 1) and the hPMS2 protein (Fig. 2; SEQ ID NO:13). This gene was found to be homologous (48% identity) to the human *PMS2* (SEQ ID NO:3) cDNA and its encoded polypeptide (31% identity) (Figure 2). Other homologs to the *ATPMS2* were also identified from blast searching sequence databases. One mutL homolog is closely related to the MLH1 mammalian homolog and is referred to as ATMLH1 (shown in Fig. 3) and another is closely related to the mammalian PMS1 polypeptide referred to as ATPMS1 (shown in Fig. 4). A phylogenetic tree is shown in Fig. 5 showing the homology of the mutL homologs to the human *PMS2* gene.

Degenerate primers can be used for isolating MMR genes from other plant species in a similar fashion.

EXAMPLE 2: Generation Of Dominant Negative Alleles Of Plant Mismatch Repair Genes

To demonstrate that putative plant MMR proteins are truly involved in MMR biochemical process, cDNAs are cloned into constitutive (31,32) or inducible (33) bacterial expression vectors for functional studies.

Various deletion mutants are generated to produce dominant negative MMR genes. Dominant negative alleles that are identified in the bacterial system are then useful for plant studies. Dominant negative MMR genes are prepared by over-expression of full-length MMR genes or by deletion analysis using standard protocols used by those skilled in the art of molecular biology. One such dominant MMR gene mutant was created by generating a construct with similar domains to that of the human dominant negative PMS2 gene (referred to as PMS134) (13, U.S. Patent No. 6,146,894). To generate this vector, the ATPMS2 (SEQ ID NO: 4) and hPMS2 cDNA (SEQ ID NO: 3) sequences were aligned and the conserved domain was isolated. Figure 6 shows a sequence alignment between the human and AT PMS134 cDNAs where a 52% identity is found between the two sequences. At the protein level these domains have a 51% identity (Figure 7). Dominant negative hPMS134 and ATPMS134 genes were made by PCR and subcloned into bacterial expression vectors. The ATPMS134 was generated by PCR from the cloned cDNA using a sense primer (SEQ ID NO:1) corresponding to the N-terminus and an antisense primer (SEQ ID NO:5) 5'gtcgacttatcacttgtcatcgtcgtccttgtagtcgagcgtagc-aactggctc-3' centered at nt 434 of the ATPMS2 cDNA (SEQ ID NO:4). This primer also contains a flag epitope that will allow protein detection followed by two termination codons. PCR products of the expected molecular weight were gel purified and cloned into T-tail vectors. Recombinant clones were sequenced to ensure authentic sequences. Inserts were then cloned into the inducible pTAC expression vector, which also contains the Ampicillin resistance gene as a selectable marker. The human PMS134 allele was also cloned into the pTAC expression vector as a positive control. Electrocompetent DH5alpha and DH10b bacterial cells (Life Technologies) were electroporated with empty vector, and the loaded vectors pTACATPMS134 and pTAChPMS134, using an electroporator (BioRAd) following the manufacturer's protocol. Bacterial cultures were then plated on to LB agar plates containing 100μg/ml ampicillin and grown

at 37°C for 14 hours. Ten recombinant clones were then isolated and grown in 5 mls of LB broth containing 50 μg/ml ampicillin plus 50μM IPTG for 18 hr at 37°C. One hundred microliters were then collected, spun down, and directly lysed in 2X SDS buffer for western blot analysis. For western analysis, equal number of cells were lysed directly in 2X SDS buffer (60 mM Tris, pH 6.8, 2% SDS, 10% glycerol, 0.1 M 2-mercaptoethanol, 0.001% bromophenol blue) and boiled for 5 minutes. Lysate proteins are separated by electrophoresis on 4-12% NuPAGE gels (Novex). Gels are electroblotted onto Immobilon-P (Millipore) in 48 mM Tris base, 40 mM glycine, 0.0375% SDS, 20% methanol and blocked overnight at 4°C in Tris-buffered saline plus 0.05% Tween-20 and 5% condensed milk. Filters are probed with a polyclonal antibody generated against MMR polypeptide sequence or a fused tag (e.g. FLAG, HIS, etc.) and a horseradish peroxidase conjugated secondary antibody, using chemiluminescence for detection (Pierce). Figure 8 shows a western blot of a clone that expresses the human PMS134 protein (Figure 8A, lane 2) using a human PMS2-specific antibody (directed to residues 2-20) of the hPMS134 sequence (see Fig. 1, and SEQ ID NO:6) or the Arabidopsis PMS134 protein (Figure 8B, lane 2) using an anti-FLAG antibody directed to the fusion residues at the C-terminus of the protein. Cells expressing empty vector had no detectable expression.

Bacterial clones expressing the h*PMS134, ATPMS134* or the empty vector were grown in liquid culture for 24 hr at 37°C in the presence of 50 μg/ml ampicillin plus 50μM IPTG. The next day, cultures were diluted 1:10 in medium containing 50μM IPTG plus ampicillin or ampicillin plus 25 μg/ml kanamycin (AK) and cultures were grown for 18 hr at 37°C. The following day, a 0.1 μl aliquot (2 μl diluted in 1000 μl of LB medium and used 50 μl for plating) of cells grown in Amp medium were plated on LB-agar plates containing 40 μg/ml of 5-bromo-4-chloro-3-indolyl-B-D-galactoside (X-gal) plus 100μg/ml ampicillin (AMP), while a 1 μl aliquot (1 μl diluted in 100 μl of LB medium and used 100 μl for plating) of cells

grown in AK medium were plated on LB-agar plates containing X-gal and 50μg/ml kanamycin (KAN). Plates were incubated for 18 hours at 37°C. The results from these studies show that cells expressing the hPMS134 or the ATPMS134 polypepetides displayed increased mutation rates in the genome of the DH10B bacterial strain which resulted in the production of KAN resistant clones (Figure 9). Following the mutagenesis protocol described above, bacterial cells expressing the plant ATPMS134 were found to have an increase in the number of KAN resistant cells (12 clones) in contrast to cells expressing the empty vector, which yielded no KAN resistant clone. These data demonstrate that dominant negative *ATPMS134* MMR genes are useful for creating hypermutable organisms that can generate phenotypically diverse offspring when put under selective conditions. Moreover, these data demonstrate that plants also use the conserved MMR process for genomic stability.

Dominant negative plant MMR gene mutants are also analyzed using mammalian cell systems. In this case, plant MMR gene cDNAs are cloned into eukaryotic expression vectors as described (13,34) and cells expressing dominant negative mutants are analyzed by measuring stability of endogenous microsatellite markers and biochemical activity of cell extracts from lines expressing dominant negative MMR gene alleles. Such methods are known by those skilled in the art and previously described (13).

EXAMPLE 3: Inhibition Of Plant MMR Activity By Dominant Negative MMR Alleles Produces Genetic Hypermutability And Microsatellite Instability.

Dominant negative alleles of human and AT MMR genes identified using bacterial and or mammalian systems can be used for plants. To test the hypothesis that dominant negative MMR gene

alleles produce global hypermutability in plants, the hPMS134 and ATPMS134 cDNAs were expressed in plants. These alleles have been found to work across species where the introduction of these genes into MMR proficient bacterial or mammalian cells renders the cells MMR deficient. Assays to carry out these studies are described below.

Engineering plant expression vectors to express the PMS134 dominant negative alleles.

A BamH I fragment containing the hPMS134 cDNA was obtained from the pSG5PMS134 plasmid (ref 13) and cloned into the corresponding sites of the pEF1/SP1-V5 vector (InVitrogen). The resulting vector (pEF-PMS134-sense) was then digested with Pme I to release a blunted DNA fragment containing the PMS134 cDNA. This fragment was then subcloned into the blunt Sma I and EcoICR I sites of the pGPTV-KAN binary plant expression vector (American Type Culture Collection). One clone, named pCMV-hPMS134-Kan (see figure 10), was sequenced to confirm that the vector contained authentic promoter and gene insert sequences. A schematic diagram of the pCMV-hPMS134-Kan vector is shown in Figure 10.

Generation of hPMS134-Expressing Arabidopsis thaliana transgenic plants.

Agrobacterium tumefaciens cells (agrobacteria) are used to shuttle genes into plants. To generate PMS134-expressing Arabidopsis thaliana (A. thaliana) plants, *Agrobacterium tumefaciens* cells (strain GV3101) were electroporated with pCMV-hPMS134-Kan or the pBI-121 (BRL) control binary vector. The pBI-121 control contains the CaMV promoter driving the expression of the β-glucuronidase cDNA (GUS) and serves as a control. Both vectors carry the neomycin phosphotransferase (NPTII) gene that allows selection of agrobacteria and plants that contain the expression vector. One-month old A. thaliana (ecotype Columbia) plants were infected

by immersion in a solution containing 5% sucrose, 0.05% silwet, and binary vector-transformed agrobacteria cells for 10 seconds. These plants were then grown at 25^{0}C under a 16 hour day and 8 hour dark photoperiod. After 4 weeks, seeds (referred to as T1) were harvested and dried for 5 days at 4°C. Thirty thousands seeds from ten CMV-hPMS134-Kan-transformed plants and five thousand seeds from two pBI-121-transformed plants were sown in solid Murashige and Skoog (MS) media plates in the presence of 50 μg/ml of kanamycin (KAN). Three hundred plants were found to be KAN resistant and represented PMS134 expressing plants. These plants along with 300 control plants were grown in MS media for two weeks and then transferred to soil. Plants were grown for an additional four weeks under standard conditions at which time T2 seeds were harvested.

To confirm the integration and stability of the PMS134 gene in the plant genome, gene segregation and PCR analyses were conducted. Commonly, three out of four T1 plants transformed by agrobacteria technology are expected to carry the vector inserted within a single locus and are therefore considered heterozygous for the integrated gene. Approximately 75% of the seeds (T2) generated from most of the T1 plants were found KAN–resistant and this in accordance with the expected 1:2:1 ratio of null (no hPMS134 containing plants), heterozygous, and homozygous plants, respectively, in self-pollinating conditions. To confirm that these plants contained the hPMS134 expression vector, genomic DNA was isolated from leaves of T1 plants using the DNAzol-mediated technique following the manufacturer's suggestion (BRL-Life Technologies). One nanogram of genomic DNA was analyzed by polymerase chain reaction (PCR) to confirm the presence of the hPMS134 gene. PCR was carried out for 25 cycles with the following parameters: 95^{0}C for 30 seconds; 55^{0}C for 1 minute; and 72^{0}C for 2 minutes using hPMS134-specific sense (SEQ ID NO: 7: 5'-tct aga cat gga gcg agc tga gag ctc-3') and antisense (SEQ ID NO: 8: 5'-tct aga agt tcc aac ctt cgc cga tgc-3') primers. Positive reactions were observed in DNA from pCMV-

hPMS134-Kan-transformed plants and not from pBI-121-transformed plants, thus confirming the integration of this vector.

In order to assess the expression of hPMS134 in T1 plants, leaf tissue was collected from T1 plants, homogenized in liquid nitrogen using glass pestles, and suspended in RLT lysing buffer (Qiagen, RNeasy plant RNA extraction kit). Five micrograms of total RNA was purified according to the manufacturer's suggested protocol and then loaded onto a 1.2% agarose gel (1x MOPS buffer, 3% formaldehyde), size-fractionated by electrophoresis, and transferred onto N-Hybond+ membrane (Amersham). Each membrane was incubated at 55^0C in 10 ml of hybridization solution (North2South labeling kit, Pierce) containing 100 ng of PMS134, tubulin, or KAN cDNA probes, which were generated by PCR amplification, according to the manufacturer's directions. Membranes were washed three times in 2x SSC, 0.1% SDS at 55^0C, and three times in 2x SSC at ambient temperature. Detection was carried out using enhanced chemiluminescence (ECL). Expression was also carried out by reverse trascriptase PCR as described above using polyA isolated mRNA that was isolated over a oligo dT column (Qiagen). A representative example of these studies are shown in figure 11. Here hPMS134 expression was detected in three out of ten analyzed pCMV-hPMS134-Kan transgenic lines, while no signal was found in the ten pBI-121 transformed plants analyzed. Immunoblot using whole lysates is used to confirm protein expression. Collectively these studies demonstrate the generation of hPMS134 expressing transgenic A. thaliana plants.

Molecular Characterization of PMS134-Expressing Plants.

MMR is a process that is involved in correcting point mutations and "slippage" mutations within repetitive mono-, di-, and tri-nucleotide (microsatellite) repeats that occur throughout the genome of an organism after cellular replication. This process is very similar to a computer spell

check function. The inactivation of MMR has been shown to result in global genomic hypermutation whereby cells with defective MMR experience over a one thousand-fold increase in point mutations and microsatellite instability (MI) (mutations within repetitive sequences) throughout their genomes per division. (35). MMR deficiency is the only known process capable of producing MI and has been used as a marker to detect cells with MMR dysfunction (36). Microsatellites serve as molecular tools to measure the inactivation of MMR that occurs by the defective MMR due to but not limited to expression of dominant negative MMR genes, double stranded RNA interference vectors, or inhibition by antisense nucleotides, or by gene knockout. In *A. thaliana*, a series of poly-A (A)n, (CA)n and (GA)n sequences were identified from genome searches using EMBL and GenBank databases. To demonstrate that hPMS134 expression could produce MI in *A. thaliana*, we analyzed microsatellites in T1 plants by PCR analyses. Initially we monitored three microsatellites, ATHACS, Nga280, and Nga128 with published primers that have been previously used to map the Arabidopsis genome (37). Briefly, DNA was extracted from A. thaliana leaves as described above. 10 ngs of plant genomic DNA was used as template for PCR amplification using the following amplification conditions: 94^{0}C for 15 sec, 55^{0}C for 15 sec and 72^{0}C for 30 seconds. PCR products were analyzed on 5% Metaphor agarose (BioWhittaker Molecular Applications) and ethidium bromide staining. In one transgenic pCMV-PMS134-Kan line, we detected a double product, likely representing a new allele of the polymorphic nga280 locus (Figure 12). These data demonstrate the ability to produce MMR deficiency and MI in plants expressing the hPMS134 dominant negative allele and provide a molecular tool for screening MMR-defective plants.

Biochemical assays for mismatch repair. MMR activity in nuclear extracts is performed as described, using 24 fmol of substrate as described (13). Complementation assays are done by adding ~ 100 ng of purified MutL or MutS components to 100 μg of nuclear extract, adjusting the final

KCl concentration to 100 mM. The substrates used in these experiments will contain a strand break 181 nucleotides 5' or 125 nucleotides 3' to the mismatch.

EXAMPLE 4: Inactivation Of MMR Leads To Plants With New Phenotypes.

We demonstrated the ability of the defective MMR to produce molecular changes within plants. The objective of this section is to demonstrate the ability to generate MMR defective plants with macroscopic output traits. One way to measure for plants with new phenotypes is to grow plants under toxic conditions, such as but not limited to high levels of toxic ions, pest-infection, drought conditions, or extreme temperatures to identify a minority of plants with new output traits, *i.e.*, resistance. Another way to score for plants with new phenotypes is through physical differences of MMR defective plants grown in standard conditions. An example of MMR-defective plants with new phenotypes include the generation of plants with double shoot apical meristems (Figure 13) as well as plants with altered chlorophyll production rendering plants albino (data not shown). In Figure 13, we show a typical wild type plant (left, labeled normal) and a plant produced from the MMR defective group (right, labeled MMR deficient). The double-meristem trait was not observed in greater than 500 normal plants. The double-meristem trait does not appear to be due to transgene integration since segregation analysis reveals the ability to generate double-meristem plants in the absence of transgene positive plants while MMR proficient control plants with other transgene vectors (pBI-121) did not produce this phenotype (data not shown). These data suggest that defective MMR produced a mutation or mutations within the plant genome that altered the normal biochemical function of the host to produce a new output trait.

These data demonstrate the ability to create plant subtypes with new

genetic and phenotypic traits by blocking the endogenous MMR process of the plant cell or whole organism.

EXAMPLE 5: Inhibition of Plant MMR Activity Using Molecular Approaches.

This application teaches of the use of inhibiting MMR activity in a plant to produce genetically altered offspring with new phenotypes.

The inhibition of MMR activity in a host organism can be achieved by introducing a dominant negative allele as shown in Figure 11 and 12. Other ways to suppress MMR activity of a host is by: knocking out alleles of a MMR protein through homologous recombination (38); blocking MMR protein dimerization with other subunits (which is required for activity) by the introduction of polypeptides into the host via transfection methods; knocking out the expression of a MMR gene using anti-sense oligonucleotides (20), and/or the use of double stranded RNA interference genes (21).

MMR gene knockouts.

Data shown in EXAMPLE 1 demonstrate that plants contain MMR gene homologs that can be genetically engineered to produce altered biochemical activities. Data presented in EXAMPLES 3 and 4 demonstrate that defective MMR in plants can produce hypermutable parental plants and offspring. Together, these data demonstrate that inhibiting endogenous MMR genes by targeting vectors of the particular MMR gene can lead to hypermutability of a plant host that generate offspring with altered genetic loci and/or new phenotypes as described in EXAMPLES 3, 4, and 5. Hypermutable seedlings can also be produced with "knocked out" MMR genes using methods known by those skilled in the art. These can be used to produce genetically diverse offspring for commercial and medical

applications (38). Cells will be confirmed to have lost the expression of the MMR gene using standard northern techniques and determined to be MMR defective using microsatellite analysis as described in EXAMPLE 3.

Blocking polypeptides.

MMR subunits (MutS and MutL proteins) interact to form active MMR complexes. Peptides are able to specifically inhibit the binding of two proteins by competitive inhibition. Isolation of plant MMR genes allows for the elucidation of primary amino acid structures as described in EXAMPLE 1. Peptides containing some but not all of the domains can be synthesized from domains of the particular MMR gene and introduced into host plants using methods known by those skilled in the art (22). Like truncated PMS134, such peptides will compete with functional full length proteins for binding and form enzymatically inactive MMR complexes. The data indicate that the domains which are C-terminal to the 134 position in human PMS2 are dispensible for binding and necessary for enzymatic activity. As shown herein, a similar domain structure is also found in plant PMS2. Seedlings exhibiting hypermutability will be useful to produce genetically diverse offspring for commercial and medical applications.

RNA blockade and Double Stranded Interference.

MMR subunits (MutS and MutL proteins) interact to form active MMR complexes. Peptides are able to specifically inhibit the binding of two proteins by competitive inhibition. Antisense oligonucleotides are synthesized against the cDNA sequence of plant MMR homologs identified in EXAMPLE 1 (20). Antisense molecules are then introduced into host plants using methods described in EXAMPLE 2 or through the bathing of seedlings or plantlets. Seedlings exhibiting hypermutability will be useful to produce genetically diverse offspring for commercial and medical applications.

Double stranded interference vectors are also useful for blocking expression/function of a plant MMR gene. The plant gene is expressed in both sense and antisense orientations from a transfection vector and the endogenous gene expression is suppressed by endogenous silencing processes (21).

Discussion

Plants contain MMR genes that code for MMR functional proteins. Expression of dominant negative plant MMR proteins results in an increase in microsatellite instability and hypermutability in plants. This activity is due to the inhibition of MMR biochemical activity in these hosts.
The data provided within this application demonstrates the blockade of MMR in a plant to produce genetic changes that lead to the production of offspring or cells with new output traits. This method is applicable to generate crop plants with new output traits as well as plant cells exhibiting new biochemicals for commercial use.

References cited (each of which is expressly incorporated herein for all purposes)

1. Liu, B., Parsons, R., Papadopoulos, N., Nicolaides, N.C., Lynch, H.T., Watson, P., Jass, J.R., Dunlop, M., Wyllie, A., Peltomaki, P., de la Chapelle, A., Hamilton, S.R., Vogelstein, B., and Kinzler, K.W. 1996. Analysis of mismatch repair genes in hereditary non-polyposis colorectal cancer patients. Nat. Med. 2:169-174.
2. Bronner, C.E., Baker, S.M., Morrison, P.T., Warren, G., Smith, L.G., Lescoe, M.K., Kane, M., Earabino, C., Lipford, J., Lindblom, A., Tannergard, P., Bollag,R.J., Godwin, A., R., Ward, D.C., Nordenskjold, M., Fishel, R., Kolodner, R., and Liskay, R.M. 1994. Mutation in the DNA mismatch repair gene homologue *hMLH1* is associated with hereditary non-polyposis colon cancer. Nature 368:258-261.

3. Leach, F.S., Nicolaides, N.C, Papadopoulos, N., Liu, B., Jen, J., Parsons, R., Peltomaki, P., Sistonen, P., Aaltonen, L.A., Nystrom-Lahti, M., Guan, X.Y., Zhang, J., Meltzer, P.S., Yu, J.W., Kao, F.T., Chen, D.J., Cerosaletti, K.M., Fournier, R.E.K., Todd, S., Lewis, T., Leach R.J., Naylor, S.L., Weissenbach, J., Mecklin, J.P., Jarvinen, J.A., Petersen, G.M., Hamilton, S.R., Green, J., Jass, J., Watson, P., Lynch, H.T., Trent, J.M., de la Chapelle, A., Kinzler, K.W., and Vogelstein, B. 1993. Mutations of a *mutS* homolog in hereditary non-polyposis colorectal cancer. Cell 75:1215-1225.

4. Nicolaides, N.C., Papadopoulos, N., Liu, B., Wei, Y.F., Carter, K.C., Ruben, S.M., Rosen, C.A., Haseltine, W.A., Fleischmann, R.D., Fraser, C.M., Adams, M.D., Venter, C.J., Dunlop, M.G., Hamilton, S.R., Petersen, G.M., de la Chapelle, A., Vogelstein, B., and kinzler, K.W. 1994. Mutations of two PMS homologs in hereditary nonpolyposis colon cancer. Nature 371: 75-80.

5. Nicolaides, N.C., Palombo, F., Kinzler, K.W., Vogelstein, B., and Jiricny, J. 1996. Molecular cloning of the N-terminus of GTBP. Genomics 31:395-397.

6. Palombo, F., Gallinari, P., Iaccarino, I., Lettieri, T., Hughes, M.A., Truong, O., Hsuan, J.J., and Jiricny, J. 1995. GTBP, a 160-kilodalton protein essential for mismatch-binding activity in human cells. Science 268:1912-1914.

7. Papadopoulos, N., Nicolaides, N.C., Wei, Y.F., Carter, K.C., Ruben, S.M., Rosen, C.A., Haseltine, W.A., Fleischmann, R.D., Fraser, C.M., Adams, M.D., Venter, C.J., Dunlop, M.G., Hamilton, S.R., Petersen, G.M., de la Chapelle, A.,Vogelstein, B., and kinzler,

K.W. 1994. Mutation of a mutL homolog is associated with hereditary colon cancer. Science 263:1625-1629.

8. Perucho, M. 1996. Cancer of the microsatellite mutator phenotype. Biol Chem. 377:675-684.

9. Strand, M., Prolla, T.A., Liskay, R.M., and Petes, T.D. Destabilization of tracts of simple repetitive DNA in yeast by mutations affecting DNA mismatch repair. 1993. Nature 365:274-276.

10. Ma AH, Xia L, Littman SJ, Swinler S, Lader G, Polinkovsky A, Olechnowicz J, Kasturi L, Lutterbaugh J, Modrich P, Veigl ML, Markowitz SD, Sedwick WD. 2000. Somatic mutation of hPMS2 as a possible cause of sporadic human colon cancer with microsatellite instability. Oncogene 19:2249-2256.

11. Parsons, R., Li, G.M., Longley, M.J., Fang, W.H., Papadopolous, N., Jen, J., de la Chapelle, A., Kinzler, K.W., Vogelstein, B., and Modrich, P. 1993. Hypermutability and mismatch repair deficiency in RER^+ tumor cells. Cell 75:1227-1236.

12. Li, G.-M., and Modrich, P. 1995. Restoration of mismatch repair to nuclear extracts of H6 colorectal tumor cells by a heterodimer of human mutL homologs. Proc. Natl. Acad. Sci. USA 92:1950-1954.

13. Nicolaides N.C. et.al. 1998. A naturally occurring hPMS2 mutation can confer a dominant negative mutator phenotype. Mol Cell Biol. 18:1635-1641.

14. Modrich, P. 1994. Mismatch repair, genetic stability, and cancer. Science 266:1959-1960.

15. Pang, Q., Prolla, T.A., and Liskay, R.M. 1997. Functional domains of the *Saccharomyces cerevisiae* Mlh1p and Pms1p DNA mismatch repair proteins and their relevance to human hereditary nonpolyposis colorectal cancer-associated mutations. Mol. Cell. Biol. 17:4465-4473.

16. Harfe, B.D., and Jinks-Robertson, S. 2000. DNA MISMATCH REPAIR AND GENETIC INSTABILITY. Annu Rev Genet 34:359-399.

17. Culligan, K.M, and Hays, J.B. 1997. DNA mismatch repair in plants. An Arabidopsis thaliana gene that predicts a protein belonging to the MSH2 subfamily of eukaryotic MutS homologs. Plant Physiol. 115:833-839.

18. Jean M, Pelletier J, Hilpert M, Belzile F, and Kunze R. 1999. mutl Plant Isolation and characterization of AtMLH1, a MutL homologue from Arabidopsis thaliana. Mol Gen Genet. 262:633-642.

19. de Wind N., Dekker, M., Berns, A., Radman, M., and Riele, H.T. 1995. Inactivation of the mouse *Msh2* gene results in mismatch repair deficiency, methylation tolerance, hyperrecombination, and predisposition to cancer. Cell 82:321-300.

20. Hackett RM, Ho CW, Lin Z, Foote HC, Fray RG, Grierson D. 2000. Antisense inhibition of the Nr gene restores normal ripening to the tomato never-ripe mutant, consistent with the ethylene receptor-inhibition model. Plant Physiol 124:1079-1086.

21. Chuang CF, Meyerowitz EM. 2000. Specific and heritable genetic interference by double-stranded RNA in Arabidopsis thaliana. Proc Natl Acad Sci U S A 97:4985-4990.

22. Takeuchi M, Ueda T, Sato K, Abe H, Nagata T, and Nakano A. 2000. A dominant negative mutant of sar1 GTPase inhibits protein transport from the endoplasmic reticulum to the golgi apparatus in tobacco and arabidopsis cultured cells. Plant J. 23:517-525.

23. Nicolaides, N.C., Carter, K.C., Shell, B.K., Papadopoulos, N., Vogelstein, B., and Kinzler, K.W. 1995. Genomic organization of the human PMS2 gene family. Genomics 30:195-206.

24. Horii, A., et.al. 1994. Cloning, characterization and chromosomal assignment of the human genes homologous to yeast PMS1, a member of mismatch repair genes. Biochem Biophys Res Commun. 204:1257-1264.

25. Moffat, A.S., 1999. Engineering plants to cope with metals. Science 285:369-370.

26. Mazur, B., Krebbers, E., and Tingey, S. 1999. Gene discovery and product development for grain quality traits. Science. 285:372-375.

27. Shintani, D., and DellaPenna, D. 1998. Elevating the Vitamin E content of plants through metabolic engineering. Science. 282:2098-2100.

28. Peng, J., Richards, D.E., Hartley, N.M., Murphy, G.P., et.al. 1999. "Green revolution" genes encode for mutant gibberellin response modulators. Nature. 256-261.

29. DellaPenna, D. 1999. Nutritional genomics: Manipulating plant micronutrients to improve human health. Science. 285:375-379.

30. Nicolaides N.C., Kinzler, K.W., and Vogelstein, B. 1995. Analysis of the 5' region of PMS2 reveals heterogenous transcripts and a novel overlapping gene. Genomics 29:329-334.

31. Murai, N., Sutton, D.W., Murray, M.G., Slightom, J.L., Merlo, D.J., et.al. 1983. Science. 222:476-???.

32. Koziel, M.G., Adams, T.L., Hazlet, M.A., et.al., 1984.J. MOL. Appl. Genet. 2:549-560.

33. Kaulen, H., Schell, J., and Kreuzaler, F. 1986. EMBO J. 5:1

34. Nicolaides, N.C., Correa, I., Casadevall, C., Travali, S., Soprano, K.J., and Calabretta, B. 1992. The Jun family members , c-JUN and JUND, transactivate the human *c-myb* promoter via an Ap1 like element. J. Biol. Chem. 267, 19665-19672.

35. Wheeler JM, Loukola A, Aaltonen LA, Mortensen NJ, and Bodmer WF. 2000. The role of hypermethylation of the hMLH1 promoter region in HNPCC versus MSI+ sporadic colorectal cancers. J. Med. Genet. 37:588-592.

36. Hoang JM, Cottu PH, Thuille B, Salmon RJ, Thomas G, and Hamelin R. 1997. BAT-26, an indicator of the replication error

phenotype in colorectal cancers and cell *lines.* Cancer Res 57:300-303.

37. Bell, C.J., et.al. Genomics, 19:137-144, 1994.

38. Gal, S., Pisan, B., Hohn, T., Grimsley, N., and Hohn, B. 1991. Genomic homologous recombination in planta. EMBO J. 10:1571-1578.